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RAW SEQUENCE LISTING   DATE: 12/18/2002
PATENT APPLICATION: US/09/783,338B   TIME: 12:10:21

Input Set : A:\ziegler.ST25.txt
Output Set: N:\CRF4\12182002\I783338B.raw

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 4 <110> APPLICANT: Ziegler, Petra
 6         Eggeling, Lothar
 8         Sahm, Hermann
10         Thierbach, Georg
13 <120> TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
14         PROCESS FOR
15         ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
18 <130> FILE REFERENCE: 21123/277066
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C--> **20 <140> CURRENT APPLICATION NUMBER: US/09/783,338B**
C--> **20 <141> CURRENT FILING DATE: 2001-02-14**
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20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.0
26 <210> SEQ ID NO: 1
28 <211> LENGTH: 2817
30 <212> TYPE: DNA
32 <213> ORGANISM: Corynebacterium glutamicum ATCC14752
34 <220> FEATURE:
36 <221> NAME/KEY: CDS
38 <222> LOCATION: (398)..(1864)
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46 tcaagccaaa aaggggcatt ttcattaaga aaatacccct ttgacctggt gttattgagc  180
48 tggagaagag acttgaactc tcaacctacg cattacaagt gcgttgcgct gccaattgcg  240
50 ccactccagc accgcagatg ctgatgatca acaactacga atacgtatct tagcgtatgt  300
52 gtacatcaca atggaattcg gggctagagt atctggtgaa ccgtgcataa acgacctgtg  360
54 attggactct ttttccttgc aaaatgtttt ccagcgg atg ttg agt ttt gcg acc  415
55                                            Met Leu Ser Phe Ala Thr
56                                            1               5
58 ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct ccg   463
59 Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro Pro
60          10              15              20
64 cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg gcc   511
65 Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val Ala
66          25              30              35
68 ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct tca   559
69 Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser Ser
70          40              45              50
72 ggt acg tca aac agt gat acc aag gtg caa gtt cga gcg gtg acc tct   607
73 Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr Ser
74 55              60              65              70
76 gcg tat ggc ctg tac tat acg cat gtg gat atc acg ttg aat acg atc   655
77 Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr Ile
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78              75              80              85
80 acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac gtg    703
81 Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn Val
82              90              95              100
84 ttt cat gtt gtg ggc aag ttg gac acc aac ttc tcc aaa ctg tct gag    751
85 Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser Glu
86              105             110             115
88 gtt gac cgt ttg atc cgt tcc att cag gct ggt gct acc ccg cct gag    799
89 Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro Glu
90      120             125             130
92 gtt gcc gag aaa att ctg gac gag ttg gag caa tcg cct gcg tct tat    847
93 Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr
94 135             140             145             150
96 ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggc gct gtt    895
97 Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala Val
98              155             160             165
100 gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt att    943
101 Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe Ile
102             170             175             180
104 acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag ggt    991
105 Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly
106             185             190             195
108 ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg ctg    1039
109 Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu
110     200             205             210
112 cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag atc    1087
113 Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile
114 215             220             225             230
116 aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca ggt    1135
117 Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly
118             235             240             245
120 ttg aca ctt gtg caa tct ctg cag gac ggc atc acg ggc gct ccg gtg    1183
121 Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val
122             250             255             260
124 aca gca agt gca cga ttt ttt gaa aca ctc ctg ttt acc ggc ggc att    1231
125 Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile
126             265             270             275
128 gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat gtc    1279
129 Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val
130     280             285             290
132 atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct aca    1327
133 Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr
134 295             300             305             310
136 ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca gtg    1375
137 Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val
138             315             320             325
140 ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act gcg    1423
141 Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala
142             330             335             340
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144 ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc ccc   1471
145 Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro
146         345             350             355
148 gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt ggt   1519
149 Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly
150         360             365             370
152 ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att gcc   1567
153 Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala
154 375             380             385             390
156 ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg tac   1615
157 Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr
158             395             400             405
160 gcc acc ttg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt   1663
161 Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val
162             410             415             420
164 gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag   1711
165 Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu
166         425             430             435
168 tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt   1759
169 Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg
170         440             445             450
172 gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag   1807
173 Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln
174 455             460             465             470
176 aat cag cgc cgg cag aga aaa cgt cca aag act aat caa aga ttc ggt   1855
177 Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly
178             475             480             485
180 aat aaa agg taaaaatcaa cctgcttagg cgtctttcgc ttaaatagcg          1904
181 Asn Lys Arg
184 tagaatatcg ggtcgatcgc ttttaaacac tcaggaggat ccttgccggc caaaatcacg  1964
186 gacactcgtc ccaccccaga atcccttcac gctgttgaag aggaaaccgc agccggtgcc  2024
188 cgcaggattg ttgccaccta ttctaaggac ttcttcgacg gcgtcacttt gatgtgcatg  2084
190 ctcggcgttg aacctcaggg cctgcgttac accaaggtcg cttctgaaca cgaggaagct  2144
192 cagccaaaga aggctacaaa gcggactcgt aaggcaccag ctaagaaggc tgctgctaag  2204
194 aaaacgacca agaagaccac taagaaaact actaaaaaga ccaccgcaaa gaagaccaca  2264
196 aagaagtctt aagccggatc ttatatggat gattccaata gctttgtagt tgttgctaac  2324
198 cgtctgccag tggatatgac tgtccaccca gatggtagct atagcatctc ccccagcccc  2384
200 ggtggccttg tcacggggct ttccccgtt ctggaacaac atcgtggatg ttgggtcgga   2444
202 tggcctggaa ctgtagatgt tgcacccgaa ccatttcgaa cagatacggg tgttttgctg  2504
204 caccctgttg tcctcactgc aagtgactat gaaggcttct acgagggctt ttcaaacgca  2564
206 acgctgtggc ctcttttcca cgatttgatt gttactccgg tgtacaacac cgattggtgg  2624
208 catgcgtttc gggaagtaaa cctcaagttc gctgaagccg tgagccaagt ggcggcacac  2684
210 ggtgccactg tgtgggtgca ggactatcag ctgttgctgg ttcctggcat tttgcgccag  2744
212 atgcgcctg atttgaagat cggtttcttc ctccacattc ccttcccttc ccctgatctg   2804
214 ttccgtcagc tgc                                                    2817
218 <210> SEQ ID NO: 2
220 <211> LENGTH: 489
222 <212> TYPE: PRT
224 <213> ORGANISM: Corynebacterium glutamicum ATCC14752
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234             20                  25                  30
237 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly
238         35                  40                  45
241 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
242     50                  55                  60
245 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
246 65                  70                  75                  80
249 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
250                 85                  90                  95
253 Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
254             100                 105                 110
257 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
258             115                 120                 125
261 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
262     130                 135                 140
265 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
266 145                 150                 155                 160
269 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
270             165                 170                 175
273 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
274             180                 185                 190
277 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
278         195                 200                 205
281 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
282     210                 215                 220
285 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
286 225                 230                 235                 240
289 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
290             245                 250                 255
293 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
294             260                 265                 270
297 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
298         275                 280                 285
301 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
302     290                 295                 300
305 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
306 305                 310                 315                 320
309 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
310             325                 330                 335
313 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe
314             340                 345                 350
317 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
318             355                 360                 365
321 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
322     370                 375                 380
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```
325 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
326 385                 390                 395                 400
329 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
330                 405                 410                 415
333 Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
334                 420                 425                 430
337 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
338             435                 440                 445
341 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
342     450                 455                 460
345 Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys
346 465                 470                 475                 480
349 Thr Asn Gln Arg Phe Gly Asn Lys Arg
350                 485
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356 <211> LENGTH: 1909
358 <212> TYPE: DNA
360 <213> ORGANISM: Corynebacterium glutamicum ATCC13032
362 <220> FEATURE:
364 <221> NAME/KEY: CDS
366 <222> LOCATION: (280)..(1746)
369 <400> SEQUENCE: 3
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374 cgccactcca gcaccgcaga tgctgatgat caacaactac gaatacgtat cttagcgtat     180
376 gtgtacatca caatggaatt cggggctaga gtatctggtg aaccgtgcat aaacgacctg     240
378 tgattggact cttttccctt gcaaatgtt ttccagcgg atg ttg agt ttt gcg      294
379                                                  Met Leu Ser Phe Ala
380                                                  1               5
383 acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct     342
384 Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
385                 10                  15                  20
387 ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg     390
388 Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
389             25                  30                  35
391 gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct     438
392 Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
393             40                  45                  50
395 tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc     486
396 Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
397     55                  60                  65
399 tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg     534
400 Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr
401 70                  75                  80                  85
403 atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac     582
404 Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
405                 90                  95                  100
407 gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct     630
408 Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
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L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date